

FIG. 1A

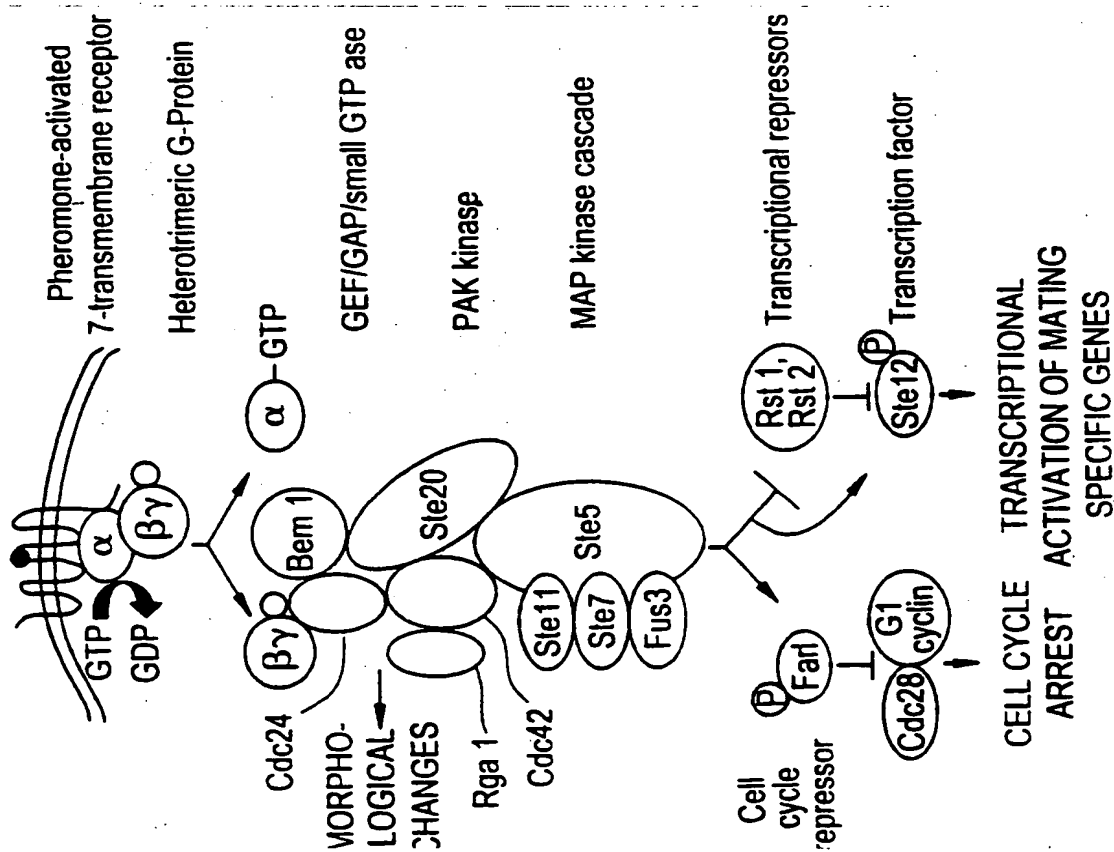


FIG. 1B

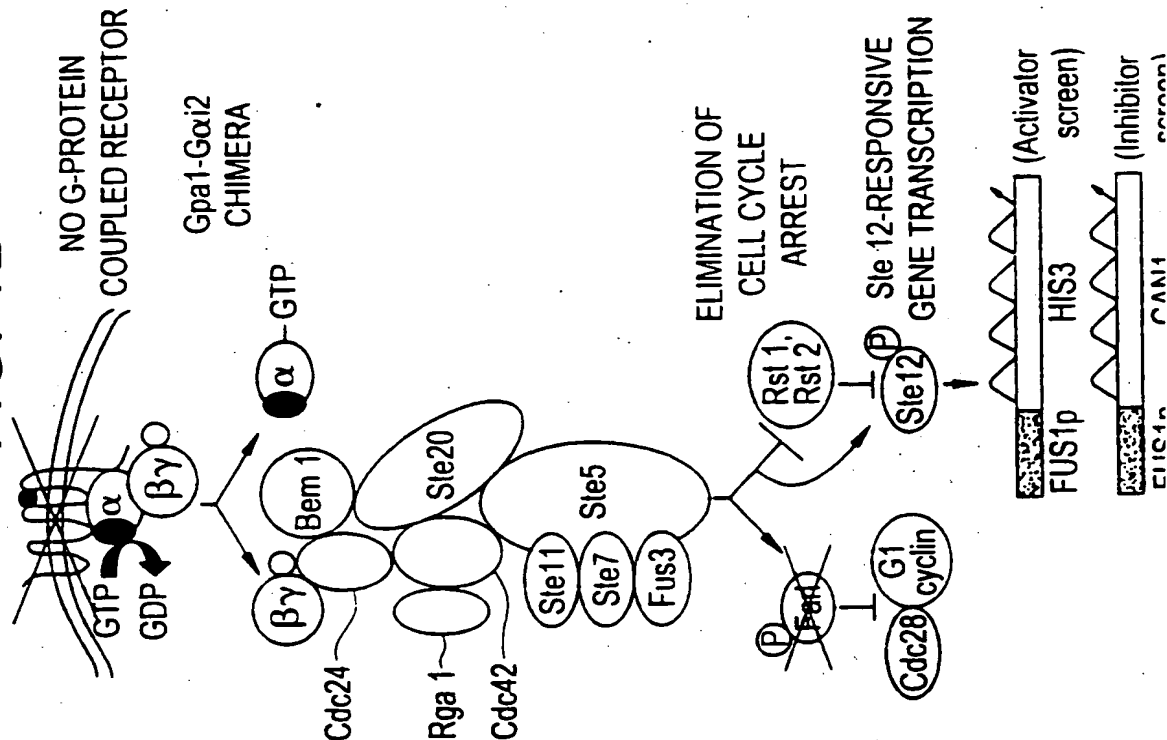


FIG. 2

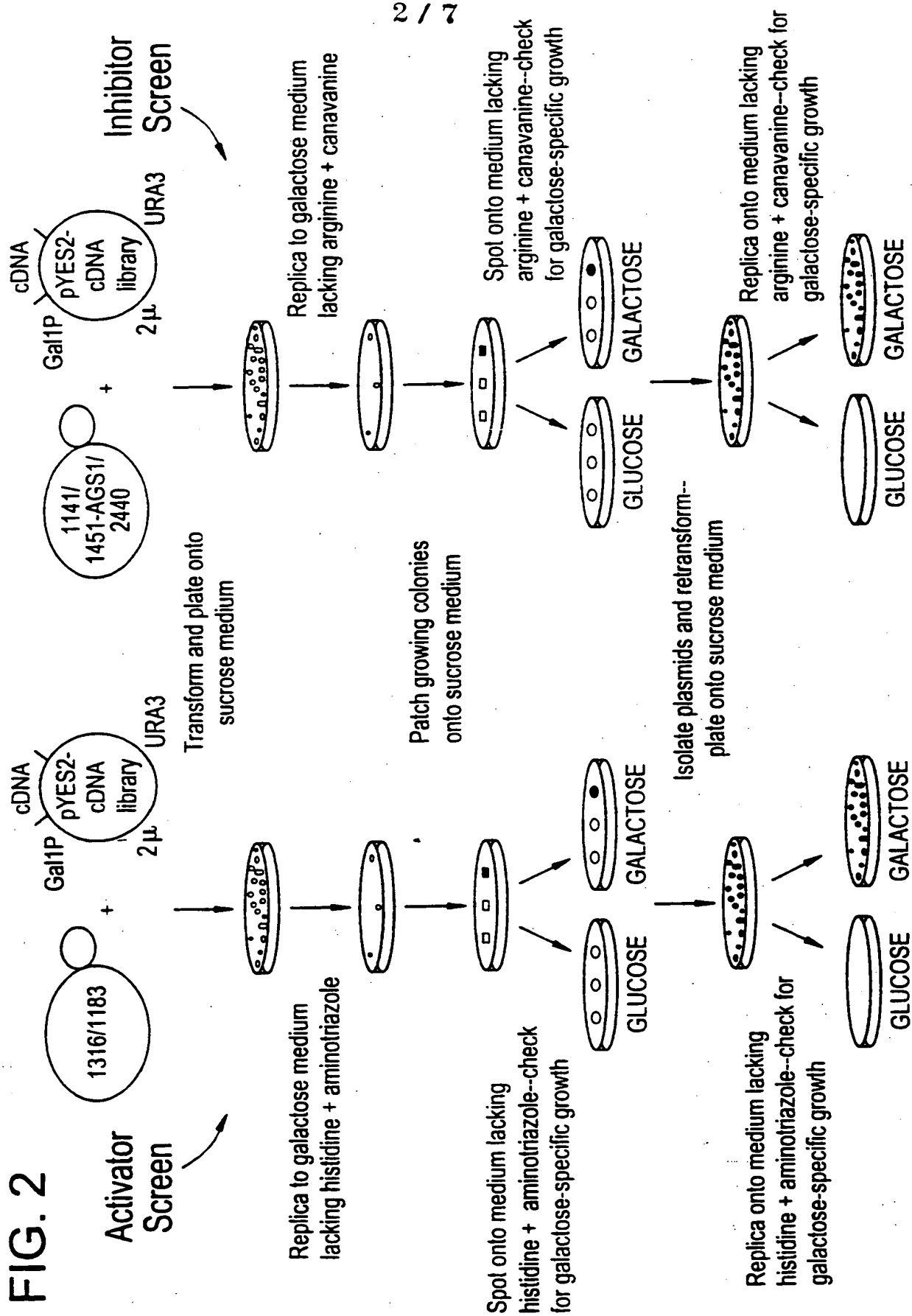


FIG. 3A

10	20	30	40	50	60
ATGAAACTGG	CCGCGATGAT	CAAGAAGATG	TGCCCGAGCG	ACTCGGAGCT	GAGTATCCCG
60					
GCCAAGAAGT	GCTATCGCAT	GGTCATCCTC	GGCTCGTCCA	AGGTGGGCAA	GACGGCCATC
120					
GTGTCCGGCT	TCCTCACCGG	CCGCTTCGAG	GACGCCTACA	CGCCTACCAT	CGAGGACTTC
180					
CACCGCAAGT	TCTACTCCAT	CCGCGGCGAG	GTCTACCAGC	TCGACATCCT	CGACACGTCC
240					
GGCAACCACC	CGTCCCGCG	CATCGGCGCG	CTCTCCATCC	TCACAGGAGA	CGTTTTTCATC
300					
310	320	330	340	350	360
CTGGTGTCA	GTCTGGACAA	CCGCGACTCC	TTCGAGGAGG	TGCAGCGGCT	CAGGCAGCAG
360					
ATCCTCGACA	CCAAGTCTTG	CCTCAAGAAC	AAAACCAAGG	AGAACGTGGA	CGTGCCCCCTG
420					
GTCATCTGCG	GCAACAAGGG	TGACCGCGAC	TTCTACCGCG	AGGTGGACCA	GCGCGAGATC
480					
GAGCAGCTGG	TGGGCGACGA	CCCCCAGCGC	TGCGCCCTACT	TCGAGATCTC	GGCCAAGAAG
540					
AACAGCAGCC	TGGACCAGAT	GTTCGCGCGG	CTCTTCGCCA	TGGCCAAGCT	GCCCAGCGAG
600					
610	620	630	640	650	660
ATGAGCCCCAG	ACCTGCACCG	CAAGTCTCG	GTGCAGTACT	GCGACGTGCT	GCACAAGAAG
660					
GCGCTGCGGA	ACAAGAAGCT	GCTGCGGGCC	GGCAGCGGCG	GCGGCGGCGG	CGACCCGGGC
720					
GACGCCTTGG	GCATCGTGCC	ACCCCTTCGCG	CGCCGGCCCCA	GCGTACACAG	CGACCTCATG
780					
TACATCCGCG	AGAAGGCCAG	CGCCGGCAGC	CAGGCCAAGG	ACAAGGAGCG	CTGCGTTCATC
840					
AGCTAG	846				

FIG.3B

MKLAAMIKKMCPSDSELSIP	AKNCYRMVILGSSKVGKTAI	40
	*	
VSRFLTGRFEDAYTPTIEDF	HRKFYSIRGEVYQLDILDT	80
	*	
GNHPFPAMRRRLSILTGDFVI	LVFSLDNRDSFEVQRLRQQ	120
*		
ILDTSCLKNKTKENVVDVPL	VICGNKGDREDFYREVDQREI	160
	*	
EQLVGDDDPQRCAYFEISAKK	NSSLDQMFRALFAMAKLPSE	200
	*	
MSPDLHRKVSQYCDVLHKK	ALRNKKLLRAGSGGGGGDPG	240
	*	
DAFGIVAPFARRPSVHSDLM	YIREKASAGSQAKDKERCVI	S 281

FIG. 4A

	PM1	G1	PM2
C-HA-RAS1	-----MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDS		
RALA	-----MAANKPKQNSLAHKKVIMVGGGVGKSALTQLQFMVDEFVEDYEPTKADS		
RAB-1A	-----MSSMPEYDYLFKLLIGDSGVGKCLLLRFADDDTYTESYISTIGVD		
RHOHP1	-----MTAAQAAGEEAPPGVRSVKVLVGDGCGKTSLLMVADGAFPESTPTVFER		
CDC42	-----MQTIKCVVVGDAVGKTCLLISYTTNKFPESEYVPTVFDN		
RAC2	-----MQAIKCVVVGDAVGKTCLLISYTTNAFPGEYIPTVFDN		
ARL1	-----MGFFSSIFSSLFGTREMRLILGLDGAGKTTILYRLQVGEVVTI-PTIGFN		
RND3/RHOE	-----MDPNQNVKCKIVVVGDSQCGKTALLHVFAKDCFPENYVPTVFEN		
AGS1	MKLAAMIKMCPDSELSIPAKNCYRMVILGSSKVGKTAIVSRFLTGRFEDAYTPTIEDF		
	: : : : *	: : : : *	: : : : *

	PM3
C-HA-RAS1	YRKQ-VVIDGETCLLDILDTAGQEYSAMRDQYMRGTGEGFLCVFAINNTKSFEDIHQYRE
RALA	YRKK-VVLDGEEVQIDILDTAGQEDYAAIRDNYFRSGEGFLCVFSITEMESEFAATADFRE
RAB-1A	FKIRTIELDGKTIKLIQIWDTAGQERFRTITSSYYRGAGHIIVVYDVTQESFNNVKQ-WL
RHOHP1	YMVN-LQVKGKPVHLHIWDTAGQDDYDRLRPLFYPDASVLLLCFDVTSFNSFDNIFNRWY
CDC42	YAVT-VMIGGEPTYLGLFDTAGQEDYDRLRPLSYPPQTDVFLVCFVSWSPSSFENVKEKWV
RAC2	YSAN-VMVDSKPVNLGLWDTAGQEDYDRLRPLSYPPQTDVFLICFSLVSPASIENVRAKWF
ARL1	VET----VTYKNLKFQVVDLGGQTSIRPYWRCYYSNTDAVIYVVDSCDRDRIGISKSELV
RND3/RHOE	YTAS-FEIDTQRIELSLWDTSGSPYDNRPLSYPDSDAVLICFDIRPETLDSVLKKWK
AGS1	HRKF-YSIRGEVYQLDILDTSNGHFFPAMRRLSILTGDFVILVFSLDNRDSFEFVQRLRQ
	: : : : *

FIG.4B

G2

C-HA-RAS1	QIKRVKD-----SDDVPMVLVGNKCDLAA-----RTVESRQAQDLARS
RALA	QILRVKE-----DENVPFLLVGNKSDLEDK-----RQVSVEEAKNRAEQ
RAB-1A	QEIDRYA-----SENVNKLVLGNKCDLTK-----KVVDYTTAKEFADS
RHOHP1	PEVNH-----CKKVPIIVVGCKTDLRKDKSLVNKLRRNGLEPVTYHRGOEMARSV
CDC42	PEITH-----CPKTPFLLVGTQIDLRDDPSTIEKLAKNKQKPIPTETAELARDL
RAC2	PEVRHH-----CPSTPIILVGTKDLRDDKDTIEKLKEKLPITYPQGLALAKEI
ARL1	AMLEEEE-----LRKAILVVFANKQDMEQAMTSSEMANSGLPALKDRK-----
RND3/RHOE	GEIQEF-----CPNTKMLLVGCKSDLRDVTSLVELSNHRQTPVSYDQGANMAKQI
AGS1	QILDTSCLKNKTKENVDPVLVICGNKGD-RDFY-----REVDPQREIEQLVGD

... : : : *

G3

C-HA-RAS1	YG--IPYIETSAKTRQG-VEDAFYTLVREIR-----
RALA	WN--VNVVETSAKTRAN-VDKVFFDLREIR-----
RAB-1A	LG--IPFLETSAKNATN-VEQSFMTMAAEIK-----
RHOHP1	GA--VAYLECSARLHDN-VHAFVQEAEEVAL-----
CDC42	KA--VKYVECSALTQRG-LKNVFDEAILAAL-----
RAC2	DS--VKYLECSALTQRG-LKTVFDEAIRAVL-----
ARL1	-----WQIFKTSATKGTG-LDEAMEWLVTLSRQ
RND3/RHOE	GA--ATYIECSALQSENSVRDIF-----HVATLAC-----VNKTNNVKNRK
AGS1	DPQRCAYFEISAKKNSS-LDQMFRALEFAMAKLPSEMSPDLHRKVSQYCDVLHKKALRNKK

... ** :

C-HA-RAS1	-----QHKLRKLNPPDES GPGCMSCKCVLS
RALA	-----ARKMEDSKEKNGKKKKRSLAKRIRERCCIL
RAB-1A	-KRMGPGATAGGA-----EKNVKIQSTPVKQAGGGCC
RHOHP1	-----SSRGRNFWRRITQGFVVT
CDC42	-----EPPETQPKRKCCIF
RAC2	-----CPQPTRQQKRACSL
ARL1	
RND3/RHOE	SQRA-----TKRISHMPSRP-----ELSAVATDLRKDKAKSCTVM

FIG.5

	P REGION		G' REGION	
RhoE/Rnd3	KIVVVGDSQCGKTALL	.	.	ISLWDTSGSPYYD
Rnd2	KIVVVGDAECGKTALL	.	.	LNWDTSGSSYYD
Rnd1	KLVLVGDVQCGKTAML	.	.	ISLWDTSGSPYYD
RhoA	KLIVVGDGACGKTCLL	.	.	LALWDTAGQEDYD
RhoB	KLIVVGDGACGKTCLL	.	.	LALWDTAGQEDYD
Cdc42	KCVVVGDGAVGKTCLL	.	.	LGLFDTAGQEDYD
Rac1	KCVVVGDGAVGKTCLL	.	.	LGLWDTAGQEDYD
H-ras	KLIVVVGAGGVGKSALT	.	.	LDILDITAGQEEYD
AGS	26 RMVILGSSKVGKTAIV	.	.	LDILDITSGNHFPF 86
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